AMENDMENT TO THE CLAIMS

Listing of Claims

The listing of claims will replace all prior versions, and listings of claims in the application.

1. (Original) A highly sensitive real-time RT-PCR capable of specifically detecting the expression of more than one MAGE gene, wherein reverse transcription of the corresponding MAGE transcripts is carried out simultaneously in a single cDNA-synthesis reaction.

2. (Original) The method of claim 1, wherein the MAGE genes are selected from the functional genes of MAGE subfamilies A, B and/or C.

3. (Previously presented) The method of claim 1, wherein the selected MAGE genes comprise MAGE-A 1, 2, 3, 4, 6, 10 and/or 12.

4. (Currently amended) The method of claim 1, wherein at least one primer for reverse transcription of MAGE mRNA is selected from the following groups of oligonucleotides:

(A)

Primer	Sequence (5′ - 3′)	SEQ ID NO
MgRT1a	CCA GCA TTT CTG CCT TTG TGA	1
MgRT1B	CCA GCA TTT CTG CCT GTT TG	2
MgRT2	CAG CTC CTC CCA GAT TT	3
MgRT3a	ACC TGC CGG TAC TCC AGG	4
MgRT3b	ACC TGC CGG TAC TCC AGG TA	5
MgRT4	GCC CTT GGA CCC CAC AGG AA	6
MgRT5a	AGG ACT TTC ACA TAG CTG GTT TCA	7
MgRT5b	GGA CTT TCA CAT AGC TGG TTT C	8
MgRT6	TTT ATT CAG ATT TAA TTT C	9

(B)

Primer	Sequence (5′ - 3′)	SEQ ID NO
Mg1_RT1	CAA GAG ACA TGA TGA CTC TC	10
Mg1_RT2	TTC CTC AGG CTT GCA GTG CA	11
Mg1_RT3	GAG AGG AGG AGG AGG TGG C	12
Mg1_RT4	GAT CTG TTG ACC CAG CAG TG	13
Mg1_RT5a	CAC TGG GTT GCC TCT GTC	14
Mg1_RT5c	CTG GGT TGC CTC TGT CGA G	15
Mg1_RT5d	GGG TTG CCT CTG TCG AGT G	16
Mg1_RT5e	GGC TGC TGG AAC CCT CAC	17
Mg1_RT6	GCT TGG CCC CTC CTC TTC AC	18
Mg1_RT7	GAA CAA GGA CTC CAG GAT AC	19

5. (Previously presented) The method of claim 1, wherein in addition to the reverse transcription of MAGE transcripts reverse transciption of a calibrator mRNA is simultaneously carried out in the same single cDNA-synthesis reaction followed by PCR-amplification of MAGE- and calibrator cDNAs.

6. (Original) The method of claim 5, wherein the calibrator mRNA is porphobilinogen desaminase (PBGD), glyceraldehyd-3-phospat dehydrogenase (GAPDH), beta-2-microglobin or beta-actin.

7. (Currently Amended) The method of claim 6, wherein the primer for reverse transcription of PBGD mRNA is selected from the following group of oligonucleotides:

Primer	Sequence (5′ - 3′)	SEQ ID NO
PBGD_RT2	CAT ACA TGC ATT CCT CAG GGT	20
PBGD_RT3	GAA CTT TCT CTG CAG CTG GGC	21
PBGD_RT4	TGG CAG GGT TTC TAG GGT CT	22
PBGD_RT10a	GGT TTC CCC GAA TAC TCC TG	23
PBGD_RT10d	TTG CTA GGA TGA TGG CAC TG	24
PBGD_RT12b	CCA AGA TGT CCT GGT CCT TG	25
PBGD_RT12c	CAG CAC ACC CAC CAG ATC	26
PBGD_RT12d	AGA GTC TCG GGA TCG TGC	27
PBGD_RT12e	AGT CTC GGG ATC GTG CAG	28
PBGD_RT12f	TCT CGG GAT CGT GCA GCA	29
PBGD_RT12g	ATG CAG CGA AGC AGA GTC T	30
PBGD_RT12h	CCT TTC AGC GAT GCA GCG	31
PBGD_RT13a	GTA TGC ACG GCT ACT GGC	32
PBGD_RT14a	GCT ATC TGA GCC GTC TAG AC	33
PBGD_RT15a	AAT GTT ACG AGC AGT GAT GC	34
PBGD_RT15b	TGG GGC CCT GCT GGA ATG	35
PBGD_RT15e	CAG TTA ATG GGC ATC GTT AAG	36
PBGD_RT15f	ATC TGT GCC CCA CAA ACC AG	37
PBGD_RT15g	GGC CCG GGA TGT AGG CAC	38
PBGD_RT15h	GGT AAT CAC TCC CCA GAT AG	39
PBGD_RT15i	CTC CCG GGG TAA TCA CTC	40
PBGD_RT15j	CAG TCT CCC GGG GTA ATC	41
PBGD_RT15k	TGA GGA GGC AAG GCA GTC	42
PBGD_RT15l	GGA TTG GTT ACA TTC AAA GGC	43

8. (Currently amended) The method of claim 5, wherien the PCR-primers for amplification of PBGD-cDNA comprises oligonucleotides selected from the following groups:

PBGD Sense Primer	Sequence (5′ - 3′)	SEQ ID NO
Hu_PBGD_se	AGA GTG ATT CGC GTG GGT ACC	44
PBGD_8	GGC TGC AAC GGC GGA AGA AAA C	45
PBGD_8_F	TGC AAC GGC GGA AGA AAA C	46
PBGD_ATG-Eco	ATG TCT GGT AAC GGC AAT GC	47
PBGD Antiense Primer	Sequence (5′ - 3′)	SEQ ID NO
PBGD_3	TTG CAG ATG GCT CCG ATG GTG AA	48
PBGD_3.1_R	GGC TCC GAT GGT GAA GCC	49
PBGD_R	TTG GGT GAA AGA CAA CAG CAT C	50

9. (Original) The method of claim 8, wherein oligonucleotides hu PBGD se and PBGD 3.1 R or hu PBGD se and PBGD R are used as primer pairs for PCR-amplification of PBGD-cDNA.

10. (Previously presented) The method of claim 1, wherein in total not more than two different oligonucleotides are used as primers for reverse transcription in the cDNA-synthesis reaction.

11. (Original) The method of claim 10, wherein the oligonucleotides MgRT3a and/or Mg1 RT5a are used as primers for reverse transcription in the cDNA-synthesis reaction.

12. (Original) The method of claim 10, wherein the oligonucleotides MgRT3a and PBGD RT15bare used as primers for reverse transcription in the cDNA-synthesis reaction.

13. (Previously presented) The method of claim 1, wherein the MAGE- and/or the calibrator-PCR are nested or semi-nested PCRs.

14. (Previously presented) The method of claim 1, wherein PCR-primers are used comprising pairs of oligonucleotides specifically amplifying only a single member of the selected group of MAGe genes, respectively.

15. (Previously presented) The method of claim 1, wherein PCR-primers are used comprising pairs of oligonucleotides comprising pairs of PCR-primers amplifying more than one member of the selected group of MAGE genes, respectively.

16. (Currently amended) The method of claim 1, wherein the PCR-primers for amplification of MAGE-cDNA comprise oligonucleotides selected from one of the following groups:

(C)

PCR-Primer	Sequence (5′ - 3′)	SEQ ID NO
MAGE-A1	GTA GAG TTC GGC CGA AGG AAC	51
MAGE-A1	CAG GAG CTG GGC AAT GAA GAC	52
MAGE-A2	CAT TGA AGG AGA AGA TCT GCC T	53
MAGE-A2	GAG TAG AAG AAG AAG CGG T	54
MAGE-A3/6	GAA GCC GGC CCA GGC TCG	55
MAGE-A3/6	GAT GAC TCT GGT CAG GGC AA	56
MAGE-A4	CAC CAA GGA GAA GAT CTG CCT	57
MAGE-A4	TCC TCA GTA GTA GGA GCC TGT	58
MAGE-A10	CTA CAG ACA CAG TGG GTC GC	59
MAGE-A10	GCT TGG TAT TAG AGG ATA GCA G	60
MAGE-A12	TCC GTG AGG AGG CAA GGT TC	61
MAGE-A12	ATC GGA TTG ACT CCA GAG AGT A	62

(D)

PCR-Primer	Sequence (5′ - 3′)	SEQ ID NO
MAGE-A1	TAG AGT TCG GCC GAA GGA AC	63
MAGE-A1	CTG GGC AAT GAA GAC CCA CA	64
MAGE-A2	CAT TGA AGG AGA AGA TCT GCC T	65
MAGE-A2	CAG GCT TGC AGT GCT GAC TC	66
MAGE-A3/6	GGC TCG GTG AGG AGG CAA G	67
MAGE-A3/6	GAT GAC TCT GGT CAG GGC AA	68
MAGE-A4	CAC CAA GGA GAA GAT CTG CCT	69
MAGE-A4	CAG GCT TGC AGT GCT GAC TCT	70
MAGE-A10	ATC TGA CAA GAG TCC AGG TTC	71
MAGE-A10	CGC TGA CGC TTT GGA GCT C	72
MAGE-A12	TCC GTG AGG AGG CAA GGT TC	73
MAGE-A12	GAG CCT GCG CAC CCA CCA A	74

17. (Original) The method of claim 16, wherein primers of group C are used for a first round and/or primers of group D for a second round of PCR-amplification.

18. (Original) The method of claim 15 carried out with a single or double pair of PCR-primers amplifying all members of the selected group of MAGE genes, respectively.

19. (Previously presented) A diagnostic composition comprising one or more suitable cDNA-primers for simultaneous reverse transcription of more than one different MAGE gene transcripts and optionally an appropriate calibrator mRNA in a single cDNA-synthesis.

20. (Original) The diagnostic composition of claim 19, wherein at least one cDNA-primer is MgRT3a, Mg1_RT5a or PBGD_RT15b.

21. (Original) An oligonucleotide selected from the following group of primers:

MgRT3a
Mg1_RT5a
PBGD_RT15b